Phyre2

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Description	P10030
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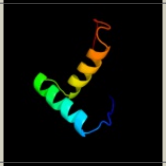
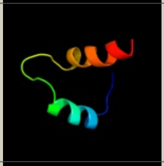
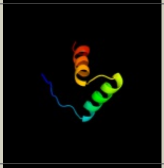
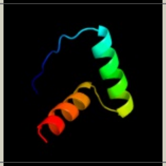
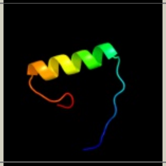
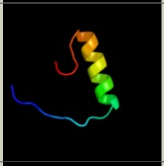
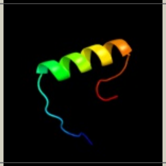
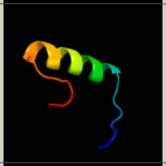
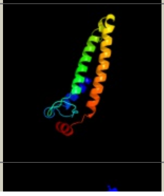
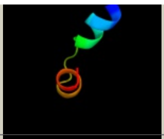
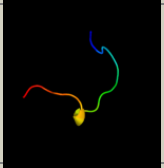
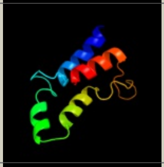
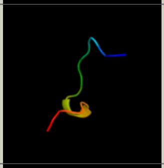
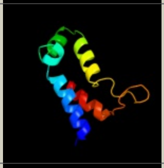
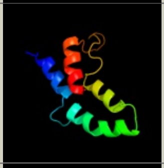
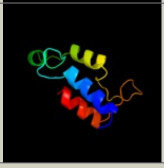
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mnta_	Alignment		89.7	30	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
2	c1u9pA_	Alignment		79.8	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
3	d1myla_	Alignment		53.5	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
4	c2kkeA_	Alignment		51.9	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
5	d1b28a_	Alignment		51.8	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
6	d1mylb_	Alignment		50.4	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
7	d1bazb_	Alignment		47.6	28	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
8	d1baza_	Alignment		45.4	28	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
9	d1bdta_	Alignment		44.8	28	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
10	d1myka_	Alignment		44.5	30	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
11	c3gtdB_	Alignment		32.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii

12	c3ns4A_	Alignment		31.3	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 53; **PDBTitle:** structure of a c-terminal fragment of its vps53 subunit suggests2 similarity of garp to a family of tethering complexes
13	d1c5ea_	Alignment		29.9	35	**Fold:**beta-clip **Superfamily:**Head decoration protein D (gpD, major capsid protein D) **Family:**Head decoration protein D (gpD, major capsid protein D)
14	c2dvlB_	Alignment		27.1	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of project tt0160 from thermus thermophilus hb8
15	c3h37B_	Alignment		26.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna nucleotidyl transferase-related protein; **PDBTitle:** the structure of cca-adding enzyme apo form i
16	d1td4a_	Alignment		24.2	29	**Fold:**beta-clip **Superfamily:**Head decoration protein D (gpD, major capsid protein D) **Family:**Head decoration protein D (gpD, major capsid protein D)
17	d1egda2	Alignment		22.7	23	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
18	c2a1tC_	Alignment		22.6	23	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase, medium-chain specific, **PDBTitle:** structure of the human mcad:etf e165betaa complex
19	c1egcB_	Alignment		19.2	23	**PDB header:**electron transfer **Chain:** B: **PDB Molecule:**medium chain acyl-coa dehydrogenase; **PDBTitle:** structure of t255e, e376g mutant of human medium chain acyl-2 coa dehydrogenase complexed with octanoyl-coa
20	c1ukwA_	Alignment		18.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of medium-chain acyl-coa dehydrogenase2 from thermus thermophilus hb8
21	c2pg0B_	Alignment	not modelled	18.1	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase from geobacillus2 kaustophilus
22	d1grja1	Alignment	not modelled	17.7	30	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
23	c3nf4B_	Alignment	not modelled	17.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to flavin adenine dinucleotide
24	c2cx9C_	Alignment	not modelled	17.1	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase
25	c2derA_	Alignment	not modelled	16.5	28	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
26	c2e7vA_	Alignment	not modelled	15.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transmembrane protease; **PDBTitle:** crystal structure of sea domain of transmembrane protease2 from mus musculus
27	d2i09a2	Alignment	not modelled	14.8	20	**Fold:**DeoB insert domain-like **Superfamily:**DeoB insert domain-like **Family:**DeoB insert domain-like
28	d3mdea2	Alignment	not modelled	14.1	22	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
						Fold: AraD/HMP-PK domain-like

29	d2pb9a1	Alignment	not modelled	14.1	32	**Superfamily:**AraD/HMP-PK domain-like **Family:**Phosphomethylpyrimidine kinase C-terminal domain-like
30	d1pp7u_	Alignment	not modelled	13.0	46	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**39 kda initiator binding protein, IBP39, N-terminal domain
31	c2rp4C_	Alignment	not modelled	12.2	50	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription factor p53; **PDBTitle:** solution structure of the oligomerization domain in dmp53
32	c2jvwA_	Alignment	not modelled	12.1	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
33	c2a5wC_	Alignment	not modelled	12.1	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
34	d1go3f_	Alignment	not modelled	12.0	30	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNA polymerase II subunit RBP4 (RpoF)
35	c1tt9B_	Alignment	not modelled	10.9	29	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
36	c2kgnA_	Alignment	not modelled	10.7	55	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein ste5; **PDBTitle:** solution structure of ste5pm24 in the zwitterionic dpc2 micelle
37	c2vigC_	Alignment	not modelled	10.3	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain specific acyl-coa dehydrogenase,; **PDBTitle:** crystal structure of human short-chain acyl coa2 dehydrogenase
38	c2pjhA_	Alignment	not modelled	10.3	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nuclear protein localization protein 4 homolog; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
39	c1rx0B_	Alignment	not modelled	10.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 8, **PDBTitle:** crystal structure of isobutyryl-coa dehydrogenase complexed2 with substrate/ligand.
40	c3ghfA_	Alignment	not modelled	9.5	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
41	c3bjqA_	Alignment	not modelled	9.2	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phage-related protein; **PDBTitle:** crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
42	c2l4uA_	Alignment	not modelled	8.9	55	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**24mer peptide from protein ste5; **PDBTitle:** solution structure of ste5pm24 in the presence of sds micelle
43	d2phpa1	Alignment	not modelled	8.9	29	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**Phosphomethylpyrimidine kinase C-terminal domain-like
44	c2jifA_	Alignment	not modelled	8.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short/branched chain specific acyl-coa dehydrogenase; **PDBTitle:** structure of human short-branched chain acyl-coa2 dehydrogenase (acadsb)
45	c2kgmA_	Alignment	not modelled	8.5	55	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein ste5; **PDBTitle:** solution structure of ste5pm24 in sds micelle
46	d1qyna_	Alignment	not modelled	8.3	17	**Fold:**SecB-like **Superfamily:**SecB-like **Family:**Bacterial protein-export protein SecB
47	c3hieA_	Alignment	not modelled	8.3	45	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex
48	c3r7kB_	Alignment	not modelled	8.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable acyl coa dehydrogenase; **PDBTitle:** crystal structure of a probable acyl coa dehydrogenase from2 mycobacterium abscessus atcc 19977 / dsm 44196
49	d1u5ea1	Alignment	not modelled	8.2	14	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
50	c2zq5A_	Alignment	not modelled	8.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
51	c2gsjA_	Alignment	not modelled	7.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ppl-2; **PDBTitle:** cdna cloning and 1.75a crystal structure determination of2 ppl2, a novel chimerolectin from parkia platycephala seeds3 exhibiting endochitinolytic activity
52	c3t38B_	Alignment	not modelled	7.6	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
53	c2kb2A_	Alignment	not modelled	7.4	27	**PDB header:**signaling protein, hydrolase regulator **Chain:** A: **PDB Molecule:**blrp1; **PDBTitle:** blrp1 bluf
						Fold: Ferredoxin-like

54	d1yrxa1	Alignment	not modelled	7.2	27	**Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
55	d1jqia2	Alignment	not modelled	7.0	18	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
56	d1v5ma_	Alignment	not modelled	6.9	5	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
57	d2ccva1	Alignment	not modelled	6.7	21	**Fold:**HPA-like **Superfamily:**Agglutinin HPA-like **Family:**Agglutinin HPA-like
58	c2p0fA_	Alignment	not modelled	6.6	23	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**rho gtpase-activating protein 9; **PDBTitle:** arhgap9 ph domain in complex with ins(1,3,5)p3
59	d1ciya3	Alignment	not modelled	6.6	23	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
60	d1ukwa2	Alignment	not modelled	6.5	23	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
61	c3oibB_	Alignment	not modelled	6.4	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of a putative acyl-coa dehydrogenase from2 mycobacterium smegmatis, iodide soak
62	d1us3a2	Alignment	not modelled	6.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
63	d1t3ta1	Alignment	not modelled	6.3	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain
64	c1mpgB_	Alignment	not modelled	6.1	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
65	d1o6da_	Alignment	not modelled	6.0	42	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
66	c2fknC_	Alignment	not modelled	5.8	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
67	c3a58A_	Alignment	not modelled	5.8	45	**PDB header:**protein transport/exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** crystal structure of sec3p - rho1p complex from2 saccharomyces cerevisiae
68	d1uwka_	Alignment	not modelled	5.8	31	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
69	c2xqyA_	Alignment	not modelled	5.8	39	**PDB header:**immune system/viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein h; **PDBTitle:** crystal structure of pseudorabies core fragment of2 glycoprotein h in complex with fab d6.3
70	d1qy9a1	Alignment	not modelled	5.5	15	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
71	d1ofcx2	Alignment	not modelled	5.4	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SLIDE domain
72	c3a9lB_	Alignment	not modelled	5.3	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
73	d1vk3a1	Alignment	not modelled	5.3	29	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
74	c1yx3A_	Alignment	not modelled	5.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
75	c2ebaI_	Alignment	not modelled	5.3	18	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**putative glutaryl-coa dehydrogenase; **PDBTitle:** crystal structure of the putative glutaryl-coa dehydrogenase from2 thermus thermophilus
76	d1miwa2	Alignment	not modelled	5.1	22	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
77	d1droa_	Alignment	not modelled	5.1	5	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
78	c2jyaA_	Alignment	not modelled	5.1	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
79	d1h4ra3	Alignment	not modelled	5.0	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM